

SEQUENCE LISTING

<110> The UAB Research Foundation

MARTIN, Michael

<120> Methods and Compositions Related to
 Regulation of Cytokine Production by Glycogen Synthase
 Kinase 3 (GSK-3)

<130> 21085.0072P1

<140> Unassigned

<141> 2005-03-09

<150> 60/551,646

<151> 2004-03-09

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 1

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Ala	Arg	Thr	Ser	Ser	Phe	Ala	Glu	Pro	Gly	Gly	Gly	Gly	Gly	Gly	Gly
			20					25					30		
Gly	Gly	Gly	Pro	Gly	Gly	Ser	Ala	Ser	Gly	Pro	Gly	Gly	Thr	Gly	Gly
		35					40					45			
Gly	Lys	Ala	Ser	Val	Gly	Ala	Met	Gly	Gly	Gly	Val	Gly	Ala	Ser	Ser
	50					55					60				
Ser	Gly	Gly	Gly	Pro	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Pro
65					70				75						80
Gly	Ala	Gly	Thr	Ser	Phe	Pro	Pro	Pro	Gly	Val	Lys	Leu	Gly	Arg	Asp
			85						90					95	
Ser	Gly	Lys	Val	Thr	Thr	Val	Val	Ala	Thr	Leu	Gly	Gln	Gly	Pro	Glu
			100					105					110		
Arg	Ser	Gln	Glu	Val	Ala	Tyr	Thr	Asp	Ile	Lys	Val	Ile	Gly	Asn	Gly
		115					120					125			
Ser	Phe	Gly	Val	Val	Tyr	Gln	Ala	Arg	Leu	Ala	Glu	Thr	Arg	Glu	Leu
	130					135					140				
Val	Ala	Ile	Lys	Lys	Val	Leu	Gln	Asp	Lys	Arg	Phe	Lys	Asn	Arg	Glu
145					150					155					160
Leu	Gln	Ile	Met	Arg	Lys	Leu	Asp	His	Cys	Asn	Ile	Val	Arg	Leu	Arg
			165					170						175	
Tyr	Phe	Phe	Tyr	Ser	Ser	Gly	Glu	Lys	Lys	Asp	Glu	Leu	Tyr	Leu	Asn
			180					185					190		
Leu	Val	Leu	Glu	Tyr	Val	Pro	Glu	Thr	Val	Tyr	Arg	Val	Ala	Arg	His
		195					200					205			
Phe	Thr	Lys	Ala	Lys	Leu	Thr	Ile	Pro	Ile	Leu	Tyr	Val	Lys	Val	Tyr
	210					215					220				

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Met Tyr Gln Leu Phe Arg Ser Leu Ala Tyr Ile His Ser Gln Gly Val
225      230      235      240
Cys His Arg Asp Ile Lys Pro Gln Asn Leu Leu Val Asp Pro Asp Thr
      245      250      255
Ala Val Leu Lys Leu Cys Asp Phe Gly Ser Ala Lys Gln Leu Val Arg
      260      265      270
Gly Glu Pro Asn Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala Pro
      275      280      285
Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val Trp
      290      295      300
Ser Ala Gly Cys Val Leu Ala Glu Leu Leu Leu Gly Gln Pro Ile Phe
305      310      315      320
Pro Gly Asp Ser Gly Val Asp Gln Leu Val Glu Ile Ile Lys Val Leu
      325      330      335
Gly Thr Pro Thr Arg Glu Gln Ile Arg Glu Met Asn Pro Asn Tyr Thr
      340      345      350
Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro Trp Thr Lys Val Phe
      355      360      365
Lys Ser Arg Thr Pro Pro Glu Ala Ile Ala Leu Cys Ser Ser Leu Leu
      370      375      380
Glu Tyr Thr Pro Ser Ser Arg Leu Ser Pro Leu Glu Ala Cys Ala His
385      390      395      400
Ser Phe Phe Asp Glu Leu Arg Cys Leu Gly Thr Gln Leu Pro Asn Asn
      405      410      415
Arg Pro Leu Pro Pro Leu Phe Asn Phe Ser Ala Gly Glu Leu Ser Ile
      420      425      430
Gln Pro Ser Leu Asn Ala Ile Leu Ile Pro Pro His Leu Arg Ser Pro
      435      440      445
Ala Gly Thr Thr Thr Leu Thr Pro Ser Ser Gln Ala Leu Thr Glu Thr
      450      455      460
Pro Thr Ser Ser Asp Trp Gln Ser Thr Asp Ala Thr Pro Thr Leu Thr
465      470      475      480
Asn Ser Ser

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<210> 2

<211> 420

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 2

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Met Ser Gly Arg Pro Arg Thr Thr Ser Phe Ala Glu Ser Cys Lys Pro
1      5      10      15
Val Gln Gln Pro Ser Ala Phe Gly Ser Met Lys Val Ser Arg Asp Lys
      20      25      30
Asp Gly Ser Lys Val Thr Thr Val Val Ala Thr Pro Gly Gln Gly Pro
      35      40      45
Asp Arg Pro Gln Glu Val Ser Tyr Thr Asp Thr Lys Val Ile Gly Asn
      50      55      60
Gly Ser Phe Gly Val Val Tyr Gln Ala Lys Leu Cys Asp Ser Gly Glu
65      70      75      80
Leu Val Ala Ile Lys Lys Val Leu Gln Asp Lys Arg Phe Lys Asn Arg
      85      90      95
Glu Leu Gln Ile Met Arg Lys Leu Asp His Cys Asn Ile Val Arg Leu
      100      105      110
Arg Tyr Phe Phe Tyr Ser Ser Gly Glu Lys Lys Asp Glu Val Tyr Leu
      115      120      125

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Asn Leu Val Leu Asp Tyr Val Pro Glu Thr Val Tyr Arg Val Ala Arg
 130 135 140
 His Tyr Ser Arg Ala Lys Gln Thr Leu Pro Val Ile Tyr Val Lys Leu
 145 150 155 160
 Tyr Met Tyr Gln Leu Phe Arg Ser Leu Ala Tyr Ile His Ser Phe Gly
 165 170 175
 Ile Cys His Arg Asp Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Asp
 180 185 190
 Thr Ala Val Leu Lys Leu Cys Asp Phe Gly Ser Ala Lys Gln Leu Val
 195 200 205
 Arg Gly Glu Pro Asn Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala
 210 215 220
 Pro Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val
 225 230 235 240
 Trp Ser Ala Gly Cys Val Leu Ala Glu Leu Leu Leu Gly Gln Pro Ile
 245 250 255
 Phe Pro Gly Asp Ser Gly Val Asp Gln Leu Val Glu Ile Ile Lys Val
 260 265 270
 Leu Gly Thr Pro Thr Arg Glu Gln Ile Arg Glu Met Asn Pro Asn Tyr
 275 280 285
 Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro Trp Thr Lys Val
 290 295 300
 Phe Arg Pro Arg Thr Pro Pro Glu Ala Ile Ala Leu Cys Ser Arg Leu
 305 310 315 320
 Leu Glu Tyr Thr Pro Thr Ala Arg Leu Thr Pro Leu Glu Ala Cys Ala
 325 330 335
 His Ser Phe Phe Asp Glu Leu Arg Asp Pro Asn Val Lys Leu Pro Asn
 340 345 350
 Gly Arg Asp Thr Pro Ala Leu Phe Asn Phe Thr Thr Gln Glu Leu Ser
 355 360 365
 Ser Asn Pro Pro Leu Ala Thr Ile Leu Ile Pro Pro His Ala Arg Ile
 370 375 380
 Gln Ala Ala Ala Ser Pro Pro Ala Asn Ala Thr Ala Ala Ser Asp Thr
 385 390 395 400
 Asn Ala Gly Asp Arg Gly Gln Thr Asn Asn Ala Ala Ser Ala Ser Ala
 405 410 415
 Ser Asn Ser Thr
 420

<210> 3

<211> 2189

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 3

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 gggccttcgg gaggcggccc tgggggctcg ggcaggcggc ggactagctc gttcgcggag 180
 cccggcgggc gaggcggagg aggcggcggc ggccccggag gctcggcctc cggcccaggc 240
 ggcaccggcg gcggaaggc atctgtcggg gccatgggtg ggggcgtcgg ggccctcgagc 300
 tccgggggtg gacccggcgg cagcggcgga ggaggcagcg gaggccccgg cgcaggcact 360
 agcttcccgc cgcccggggg gaagctgggc cgtgacagcg ggaagggtgac cacagtcgta 420
 gccactctag gccaaaggccc agagcgctcc caagaagtgg cttacacgga catcaaagtg 480
 attggcaatg gctcatttgg ggtcgtgtac caggcacggc tggcagagac cagggaacta 540
 gtcgccatca agaaggttct ccaggacaag aggttcaaga accgagagct gcagatcatg 600
 cgtaagctgg accactgcaa tattgtgagg ctgagatact ttttctactc cagtggcgag 660
 aagaaagacg agctttacct aaatctgggtg ctggaatatg tgcccagagac agtgtaccgg 720

gtggcccgcc	acttcaccaa	ggccaagttg	accatcccta	tcctctatgt	caagggtgtac	780
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tcagctggct	gtgtactggc	agagctcctc	ttggggccagc	ccatcttccc	tggggacagt	1080
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<210> 4

<211> 1639

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 4

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cttctgtggg	agaacttaat	gctgcattta	tcgttaacct	aacaccccaa	cataaagaca	180
aaaggaagaa	aaggaggaag	gaaggaaaag	gtgattcgcg	aagagagtga	tcattgtcagg	240
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tggcagcatg	aaagttagca	gagacaagga	cggcagcaag	gtgacaacag	tgggtggcaac	360
tcctgggcag	ggtccagaca	ggccacaaga	agtcagctat	acagacacta	aagtgattgg	420
aatggatca	tttgggtgtg	tatatcaagc	caaactttgt	gattcaggag	aactggtcgc	480
catcaagaaa	gtattgcagg	acaagagatt	taagaatcga	gagctccaga	tcattgagaaa	540
gctagatcac	tgtaacatag	tcggattgcg	ttatttcttc	tactccagtg	gtgagaagaa	600
agatgaggtc	tatcttaate	tgggtgctga	ctatgttccg	gaaacagtat	acagagttag	660
cagacactat	agtcgagcca	aacagacgct	ccctgtgatt	tatgtcaagt	tgtatatgta	720
tcagctgttc	cgaagtttag	cctatatcca	ttcctttgga	atctgccatc	gggatattaa	780
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aatgaacca	aactacacag	aatttaaatt	ccctcaaatt	aaggcacatc	cttggactaa	1140
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tcacactctg	gctaccatcc	ttattcctcc	tcattgctcg	attcaagcag	ctgcttcaac	1440
ccccacaaat	gccacagcag	cgtcagatgc	taatactgga	gaccgtggac	agaccaataa	1500

tgctgcttct	gcatcagctt	ccaactccac	ctgaacagtc	ccgagcagcc	agctgcacag	1560
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<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 5

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<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 6

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